We claim:

1. A method of converting a double stranded nucleic acid into a hairpin structure, wherein the double stranded nucleic acid contains at least one sequence of interest, and is referred to as the template nucleic acid, comprising either

(1) ligating a first single stranded nucleic acid to a first end of the upper strand of the template nucleic acid, and ligating a second single stranded nucleic acid which is non-complementary to the first single stranded nucleic acid to the first end of the lower strand of the nucleic acid; or

(2) ligating a cap of single stranded nucleic acid to both the upper strand and the lower strand of the first end of the template nucleic acid, wherein said cap contains a sequence about midway in the cap, and that cannot be amplified by polymerase chain reaction (PCR), and wherein the nucleic acid bases on either side of this sequence are not complementary to each other; and further comprising

ligating a cap of single stranded nucleic acid to both the lower strand and the upper strand of the second end of the nucleic acid, such that the upper strand and the lower strand of the second end are contiguous, creating the final hairpin structure.

2. A method of amplifying the hairpin structure of claim 1, comprising performing polymerase chain reaction with a first primer that binds to at least a portion of the upper single stranded non-complementary region, and a second primer that binds to at least a portion of the lower single stranded non-complementary region.

3. The method of claim 1, wherein the upper single stranded non-complementary region and the lower single stranded non-complementary region are about 20 – 40 basepairs long.

4. The method of claim 1, wherein one strand of the template nucleic acid is joined with a second, fully complementary nucleic acid strand such that the two strands are contiguous, and such that during amplification the polymerase copies both the upper strand of the template nucleic acid and the lower strand of the template nucleic acid in a single pass.

5. The method of claim 4, wherein the upper strand of the template nucleic acid is joined with the fully complementary lower strand of the template nucleic acid, such that during amplification the polymerase copies both the upper strand and the lower strand in a single pass.

6. A method of amplifying a nucleic acid sequence of interest which generates a PCR-amplified product which is substantially free of polymerase-induced errors, comprising:

(a) converting the sequence of interest into a hairpin DNA structure;

(b) amplifying the hairpin DNA using PCR with a first primer that binds to at least a portion of the upper single stranded region, and a second primer that binds to at least a portion of the lower single stranded region;

(c) converting the PCR products into hairpin structures by a method which induces denaturation followed by sudden renaturation;

(d) identifying hairpins containing polymerase-generated nucleotide changes, insertions, and deletions, via the resulting mismatched bases comprising gaps in binding, and

(e) removing such hairpin DNAs containing polymerase generated mismatched nucleotides, and collecting the DNA that contains no mismatches.

7. The method of claim 6, wherein the method which induces denaturation followed by sudden renaturation is selected from the group consisting of (a) heat denaturation followed by rapid cooling, (b) addition of sodium hydroxide followed by sudden neutralization of the solution, and (c) addition of formamide followed by sudden removal of formamide.

8. The method of claim 6, wherein the hairpin DNAs containing PCR-induced errors have a mismatch in the double stranded region and are separated from hairpin DNAs which do not contain PCR-induced errors by a method which recognizes DNA containing a mismatch.

9. The method of claim 8, wherein the method which recognizes DNA containing mismatches is selected from the group consisting of dHPLC-mediated fraction collection, denaturing gradient gel electrophoresis (DGGE), constant denaturant gel electrophoresis (CDGE), constant denaturant capillary electrophoresis (CDCE), and an enzymatic-based separation method.

10. The method of claim 9, wherein the enzymatic-based separation method is performed either in solution or bound to a solid support, and the enzyme is at least one enzyme selected from the group consisting of mismatch-recognition enzymes MutS, MutY, and TDG; Cel I; resolvases; endonuclease V; cleavases, and exonucleases.

11. The method of claim 6, wherein (a) during the course of amplification the polymerase-generated errors are converted to mismatches and remain as mismatches during each cycle of amplification, and (b) following the end of amplification all the polymerase-generated errors are in a mismatched structure while all the mutations are in a matched structure.

12. The method of claim 6, wherein one strand of the template nucleic acid is joined with a second, fully complementary nucleic acid strand such that the two strands are contiguous, and such that during amplification the polymerase copies both the upper

strand of the template nucleic acid and the lower strand of the template nucleic acid in a single pass.

13. The method of claim 12, wherein the upper strand of the template nucleic acid is joined with the fully complementary lower strand of the template nucleic acid, such that during amplification the polymerase copies both the upper strand and the lower strand in a single pass.

14. A method of amplifying a nucleic acid sequence of interest which generates a PCR-amplified product which is substantially free of polymerase-induced errors, comprising:

(a) converting the sequence of interest into a hairpin DNA structure;

(b) amplifying the hairpin DNA using PCR with a first primer that binds to at least a portion of the upper single stranded region, and a second primer that binds to at least a portion of the lower single stranded region; wherein the concentration of primers are either equal to each other ('regular PCR') or unbalanced ('asymmetric PCR');

(c) identifying hairpins containing polymerase-generated nucleotide changes, insertions, and deletions, via the resulting mismatched bases comprising gaps in binding; and

(d) removing such hairpin DNAs containing polymerase generated mismatched nucleotides, and collecting the DNA that contains no mismatches.

15. A method of improving the fidelity of an assay that relies on a PCR-amplified nucleic acid template for at least one step of the assay, wherein the PCR-amplified nucleic acid template is generated using the method of claim 6.

16. The method of claim 15, wherein the assay is selected from the group consisting of mutation detection, mutation analysis, polymorphism detection, polymorphism analysis, microsatellite analysis, cloning, and protein functional analysis.

17. The method of claim 16, wherein the method of mutation or polymorphism detection is selected from the group consisting of PCR, PCR/RE/LCR, MutEx-ACB-PCR, RFLP analysis, and APRIL-ATM.

18. A method of detecting DNA damage in a nucleic acid sequence of interest, comprising:

(a) converting the sequence of interest into a hairpin DNA structure;

(b) amplifying the hairpin DNA using PCR with a first primer that binds to at a first portion of the upper single stranded region, and a second primer that binds to a second portion of the upper single stranded region; and

(c) purifying the PCR products, wherein only those sequences of interest that contain damaged DNA are amplified.

19. A method of converting a double stranded nucleic acid into a hairpin structure, wherein the double stranded nucleic acid contains at least one sequence of interest, and is referred to as the template nucleic acid, comprising either:

a) ligating a cap of single stranded nucleic acid to both the lower strand and the upper strand of both ends of the nucleic acid, such that the upper strand and the lower strand of the second end are contiguous, creating the final hairpin structure; or

b) forming a hairpin by digesting the double stranded nucleic acid sequence with two restriction enzymes which generate different overhangs to generate a doubly digested nucleic acid with a first overhang at a first end of the nucleic acid and a second overhang at a second end of the nucleic acid; ligating a first doubly digested nucleic acid to a second, identical, doubly digested nucleic acid such that the first overhang of the first sequence ligates to the first overhang of the second sequence; and second overhang of the first sequence ligates to the second overhang of the second sequence, creating the final hairpin structure.

20. A method of amplifying a nucleic acid sequence of interest which generates an amplified product which is substantially free of polymerase-induced errors, comprising:

a) converting the sequence of interest into a hairpin structure;

b) amplifying the hairpin structure using a polymerase and primers to perform rolling circle amplification of the hairpin structure such that both the upper

strand and the lower strand are continuously amplified in succession each time the polymerase performs a full circle around the hairpin structure, generating an amplification product comprising repeated single stranded units of the sequence of interest;

c) cleaving the amplification product with a restriction enzyme to generate individual amplified nucleic acid molecules comprising a single copy of the sequence of interest each;

d) converting the amplified nucleic acid molecules into hairpin structures by a method which induces denaturation followed by sudden renaturation;

e) identifying hairpins containing polymerase-generated nucleotide changes, insertions, and deletions, via the resulting mismatched bases comprising gaps in binding; and

f) removing such hairpin DNAs containing polymerase generated mismatched nucleotides, and collecting the DNA that contains no mismatches.

21. The method of claim 20, wherein the polymerase is Phi29.

22. The method of claim 20, wherein the primers are random hexamers.

23. The method of claim 20, wherein the method which induces denaturation followed by sudden renaturation is selected from the group consisting of (a) heat

denaturation followed by rapid cooling, (b) addition of sodium hydroxide followed by sudden neutralization of the solution, and (c) addition of formamide followed by sudden removal of formamide.

24. The method of claim 20, wherein the hairpin DNAs containing polymerase-induced errors have a mismatch in the double stranded region and are separated from hairpin DNAs which do not contain polymerase-induced errors by a method which recognizes DNA containing a mismatch.

25. The method of claim 24, wherein the method which recognizes DNA containing mismatches is selected from the group consisting of dHPLC-mediated fraction collection, denaturing gradient gel electrophoresis (DGGE), constant denaturant gel electrophoresis (CDGE), constant denaturant capillary electrophoresis (CDCE), and an enzymatic-based separation method.

26. The method of claim 25, wherein the enzymatic-based separation method is performed either in solution or bound to a solid support, and the enzyme is at least one enzyme selected from the group consisting of mismatch-recognition enzymes MutS, MutY, and TDG; Cel I; resolvases; endonuclease V; cleavases, and exonucleases.

27. A method of improving the fidelity of an assay that relies on a PCR-amplified nucleic acid template for at least one step of the assay, wherein the PCR-amplified nucleic acid template is generated using the method of claim 20.

28. The method of claim 27, wherein the assay is selected from the group consisting of mutation detection, mutation analysis, polymorphism detection, polymorphism analysis, microsatellite analysis, cloning, and protein functional analysis.

29. The method of claim 28, wherein the method of mutation or polymorphism detection is selected from the group consisting of PCR, PCR/RE/LCR, MutEx-ACB-PCR, RFLP analysis, and APRIL-ATM.

30. A nucleic acid useful for amplifying a double stranded nucleic acid sequence of interest to generate an amplified product which is substantially free of polymerase-induced errors, comprising a priming structure ligated to a first end of a double stranded nucleic acid of interest, wherein the priming structure is either an oligonucleotide cap comprising a single stranded oligonucleotide that forms a hairpin structure of at least 10 nucleotides, or the priming structure comprises a pair of oligonucleotides which are complementary to each other at the ends ligated to the nucleic acid sequence of interest, and non-complementary to each other at the ends which are not ligated to the nucleic acid sequence of interest.

31. The nucleic acid of claim 30, wherein the priming structure is an oligonucleotide cap which further comprises a polymerase block at the approximate midpoint of the priming structure, wherein said polymerase block prevents polymerization by a polymerase.

32. The nucleic acid of claim 31, wherein said polymerase block is selected from the group consisting of one or more abasic nucleotides, a deoxynucleotide analogue that does not allow polymerase synthesis; and uracil.

33. The nucleic acid of claim 32, wherein the polymerase block is uracil and, following ligation to the double stranded nucleic acid sequence of interest and amplification, the cap is treated with uracil glycosylase and heat to generate a strand break.

34. A nucleic acid useful for amplifying a double stranded nucleic acid sequence of interest to generate an amplified product which is substantially free of polymerase-induced errors, comprising the nucleic acid of claim 30 ligated at a second end to a joining structure, wherein said joining structure comprises an oligonucleotide cap, wherein said oligonucleotide cap comprises a single stranded oligonucleotide that forms a hairpin structure of at least 10 nucleotides and does not contain a polymerase block.